

Figure 1

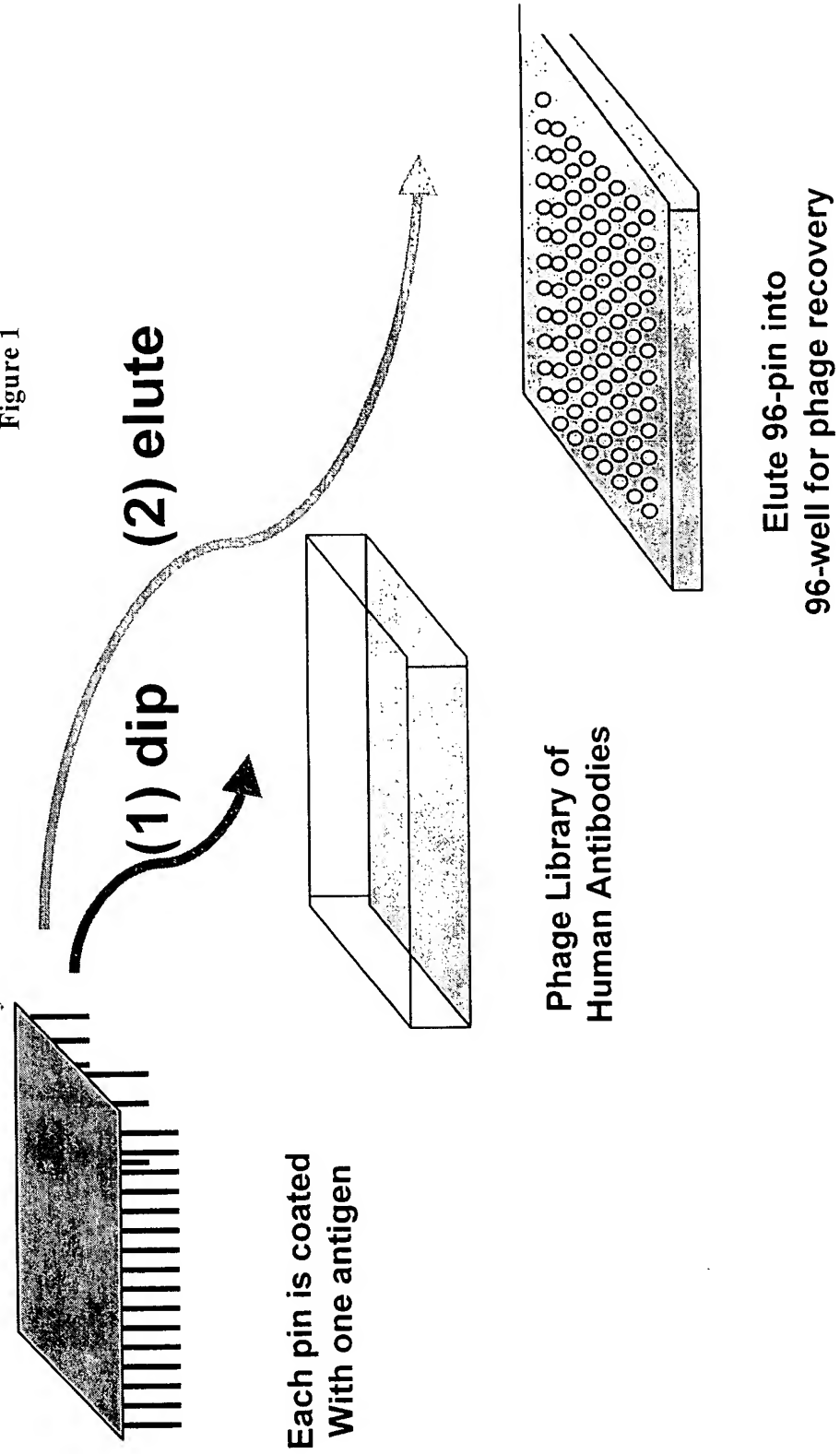


Figure 2

“ Epitope Scan” over the extracellular domain of a receptor

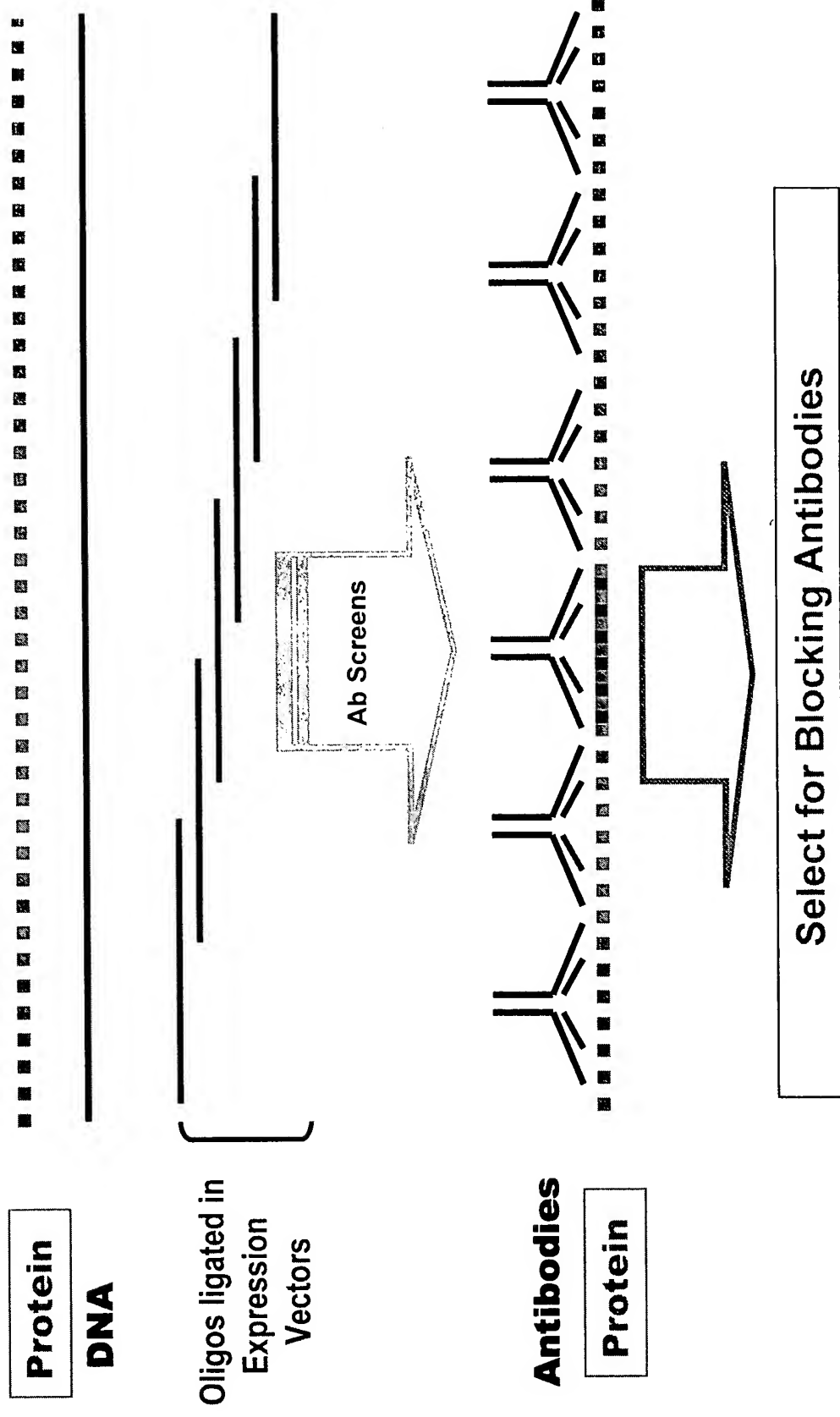


Figure 3

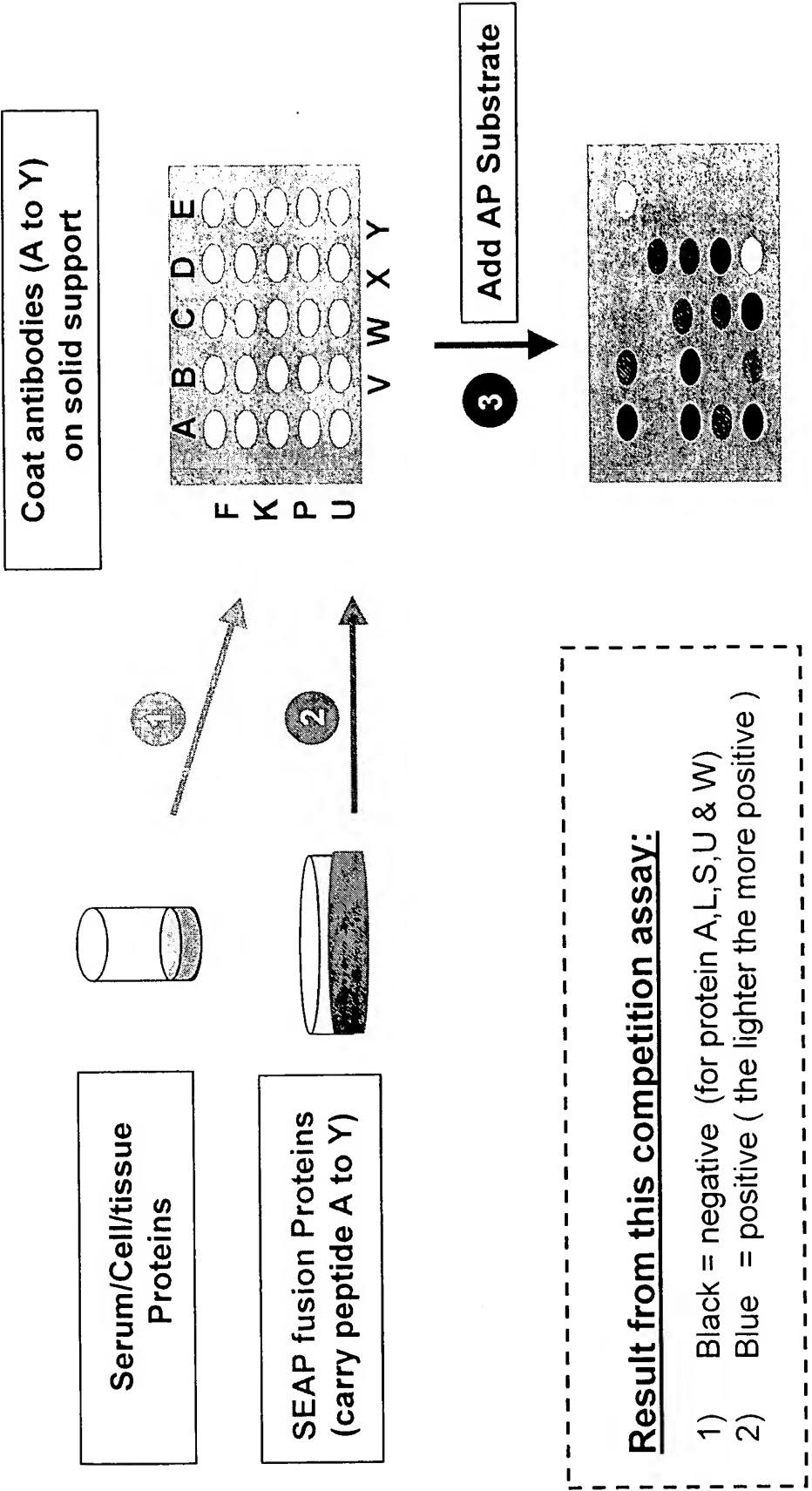


FIGURE 4

VEGF ISOFORM ALIGNMENT (VEGF-206, -165, -121)

VEGF206 = (232-26)

VEGF165 = (191-26) Missing Exon 6

VEGF121 = (147-26) Missing Exon 6 + 7

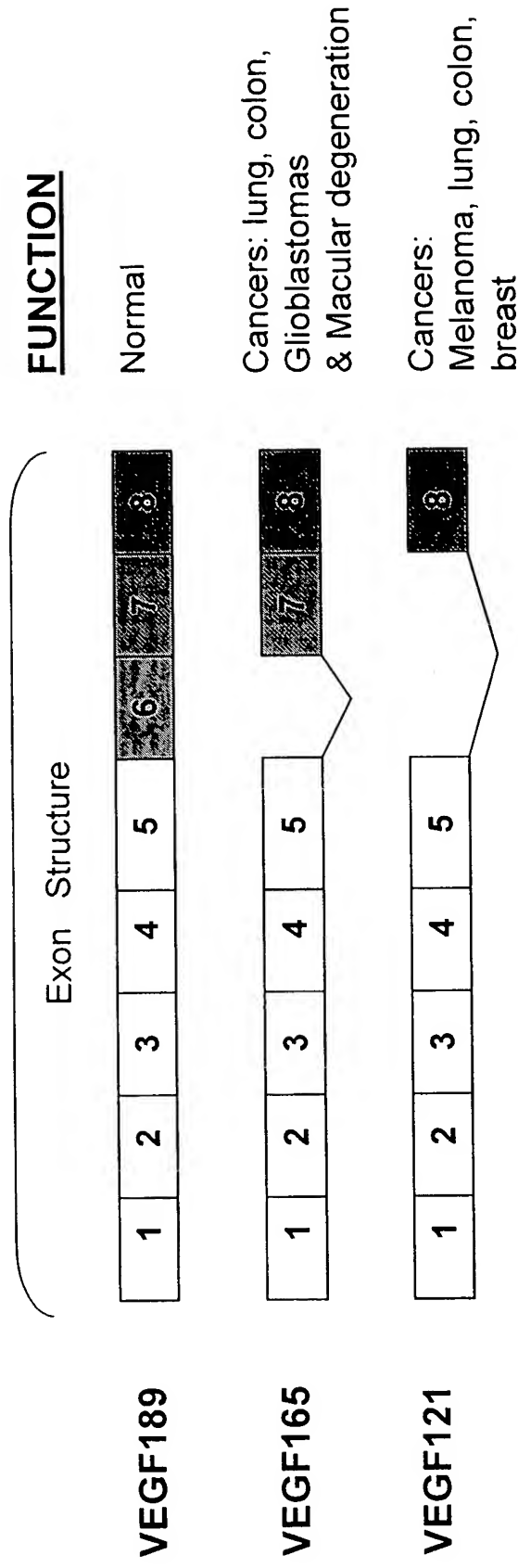
SIGNL PEPTIDE 1-26						ISOFORM

MNFLLSWVHW	SLALLLYLHH	AKWSQAAPMA	EGGGQNHHEV	VKFMDVYQRS	YCHPIETLVD	206
MNFLLSWVHW	SLALLLYLHH	AKWSQAAPMA	EGGGQNHHEV	VKFMDVYQRS	YCHPIETLVD	165
MNFLLSWVHW	SLALLLYLHH	AKWSQAAPMA	EGGGQNHHEV	VKFMDVYQRS	YCHPIETLVD	121
ANTIBODY A4.6.1						
EPITOPE REGION						

IFQEYPDEIE	YIFKPSCVPL	MRCGGCCNDE	GLECVPTES	NITMQIMRIK	PHQGQHIGEM	206
IFQEYPDEIE	YIFKPSCVPL	MRCGGCSNDE	GLECVPTES	NITMQIMRIK	PHQGQHIGEM	165
IFQEYPDEIE	YIFKPSCVPL	MRCGGCCNDE	GLECVPTES	NITMQIMRIK	PHQGQHIGEM	121
SFLQHNKCEC	RPKKDRARQE	KKSVRGKGKG	QKRKRKKSRY	KSWSVYVGAR	CCLMPWSLPG	206
SFLQHNKCEC	RPKKDRARQE					165
SFLQHNKCEC	RPKKDRARQE					121
HEPARIN BINDING DOMAIN						

PHPGPCSER	RKHLFVQDPQ	TCKCSCKNTD	SRCKARQLEL	NERTCRCDKP	RR	206
NPCGPCSER	RKHLFVQDPQ	TCKCSCKNTH	SRCKARQLEL	NERTCRCDKP	RR	165
				KCDKP	RR	121

Figure 5



SPECIFIC EPITOPES FOR VEGF ISOFORMS

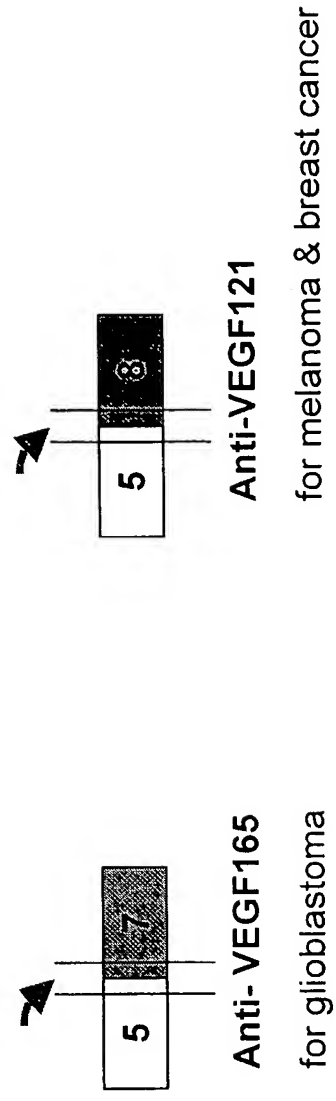


Figure 6

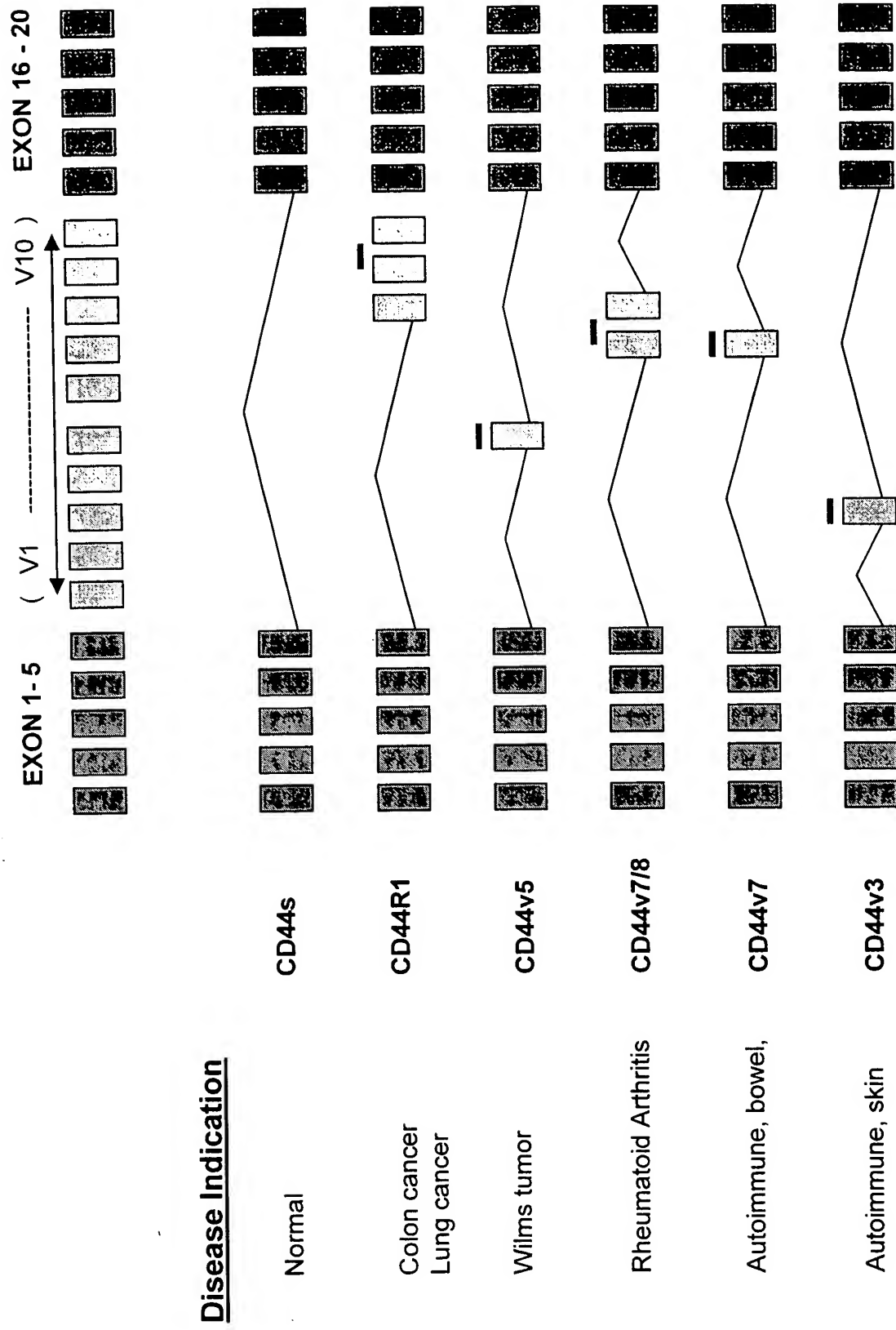


Figure 7A

tcgcgagggc ttggggcagc cgggtagctc ggaggtcgtg gcgctggggg ctagcaccag	60
cgctctgtcg ggaggcgagc cggttagggtg gaccggtcag cggactcacc ggccagggcg	120
ctcggtgctg gaatttgata ttcatatgac cgggttttat ccctcttctt ttttcttaaa	180
catttttttt taaaactgta ttgtttctcg ttttaattta tttttgcttg ccattcccca	240
cttgaatcgg gccgacggct tggggagatt gctctacttc cccaaatcac tgtggatttt	300
ggaaaccagc agaaagagga aagaggtagc aagagctcca gagagaagtc gaggaagaga	360
gagacggggg cagagagagc gcgcggggcg gcgagcagcg aaagcgacag gggcaaagtg	420
agtgcactgc ttttgggggt gaccgccgga gcgcggcggt agccctcccc cttgggatcc	480
cgcagctgac cagtcgcgct gacggacaga cagacagaca ccgccccag cccagctac	540
cacctctcc ccggccggcg gcggacagtg gacgcggcgg cgagccgcgg gcagggggcg	600
gagcccgcgc ccggaggcgg ggtggagggg gtcggggctc gcggcgctgc actgaaactt	660
ttcgtccaac ttctgggctg ttctcgcttc ggaggagccg tgggccgcgc gggggaagcc	720
gagccgagcg gagccgcgag aagtgcctagc tcgggcccgg aggagccgca gccggaggag	780
ggggaggagg aagaagagaa ggaagaggag agggggccgc agtggcgact cggcgctcgg	840
aagccgggct catggacggg tgaggcgggc gtgtgcgcag acagtgcctc agccgcgcgc	900
gctccccagg ccctggcccc ggcctcgggc cggggaggaa gagtagctcg ccgaggcgcc	960
gaggagagcg ggccgcccc aagcccagc cgagagagga gcgcgagccg cgccggcccc	1020
ggtcgggcct ccgaaacc atg aac ttt ctg ctg tct tgg gtg cat tgg agc	1071
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser	
1 5 10	
ctt gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca	1119
Leu Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala	
15 20 25	
ccc atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc	1167
Pro Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe	
30 35 40	
atg gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg	1215
Met Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val	
45 50 55	
gac atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca	1263
Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro	
60 65 70 75	

Figure 7B

tcc tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly 80 85 90	1311
ctg gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met 95 100 105	1359
cgg atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu 110 115 120	1407
cag cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa Gln His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln 125 130 135	1455
gaa aaa aaa tca gtt cga gga aag gga aag ggg caa aaa cga aag cgc Glu Lys Lys Ser Val Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg 140 145 150 155	1503
aag aaa tcc cgg tat aag tcc tgg agc gtt ccc tgt ggg cct tgc tca Lys Lys Ser Arg Tyr Lys Ser Trp Ser Val Pro Cys Gly Pro Cys Ser 160 165 170	1551
gag cgg aga aag cat ttg ttt gta caa gat ccg cag acg tgt aaa tgt Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys 175 180 185	1599
tcc tgc aaa aac aca gac tcg cgt tgc aag gcg agg cag ctt gag tta Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu 190 195 200	1647
aac gaa cgt act tgc aga tgt gac aag ccg agg cgg tga gccgggcagg Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg 205 210 215	1696
aggaaggagc ctccctcagg gtttcgg	1723

Figure 8A

aattctctgag	ctcgtctgacc	ggctcgacgag	ctc	gaggggtc	gacgagctcg	agggcgcgcg	60
cccggtcccc	accctctgca	gcaccccgcg	ccccgcgccc	tcccagccgg	gtccagccgg		120
agccatgggg	ccggagccgc	agtgagcacc	atg	gag	ctg	gcg gcc ttg tgc cgc	174
			Met	Glu	Leu	Ala Ala Leu Cys Arg	
			1			5	
tggtgg	ctctct	ctcgcc	ctcttg	ccc	ccc	gga gcc gcg agc acc caa	222
Trp Gly	Leu Leu	Leu Ala	Leu Leu	Pro Pro	Gly Ala	Ala Ala Ser Thr Gln	
	10		15			20	
gtgtgt	tgctac	accggc	acagac	atgatg	aagctg	cgcct gcc agt ccc gag	270
Val Cys	Thr Gly	Thr Asp	Met Lys	Leu Arg	Leu Pro	Ala Ser Pro Glu	
25		30			35		40
accacc	ctgtgt	gacctg	ctctcg	cac	ctctac	cagggc	tgctgt
Thr His	Leu Asp	Met Leu	Arg His	Leu Tyr	Gln Gln	Gly Cys Gln	Val Val
		45			50		55
cagcag	gga	aac	ctgtgt	gaa	ctc	acc	tac
Gln Gly	Asn Leu	Glu Leu	Thr Tyr	Leu Pro	Thr Asn	Ala Ser Leu	Ser
		60		65		70	
ttcttc	ctgtgt	caggat	atc	cag	gag	gtgtgt	cagctc
Phe Leu	Gln Asp	Ile Gln	Glu Val	Gln Gln	Gly Tyr	Val Leu	Ile Ala His
	75		80			85	
aaccaa	gtgtgt	aggcag	gtc	cca	ctgtgt	cagagg	ctgcgg
Asn Gln	Val Arg	Gln Val	Pro Leu	Gln Arg	Leu Arg	Ile Val	Arg Gly
	90		95		100		
accacc	cagctc	tttgag	gac	aac	tattgt	gcc	ctgtgt
Thr Gln	Leu Phe	Glu Asp	Asn Tyr	Ala Leu	Ala Val	Leu Asp	Asn Gly
105		110			115		120
gacgac	ccgtgt	aac	aataac	acc	acc	cctgtc	acaggg
Asp Pro	Leu Asn	Asn Thr	Thr Pro	Val Thr	Gly Ala	Ser Pro	Gly Gly
		125		130		135	
ctgtgt	cgggag	ctc	cag	ctt	cga	agc	ctc
Leu Arg	Glu Leu	Gln Leu	Arg Ser	Leu Thr	Glu Ile	Leu Lys	Gly Gly
		140		145		150	
gtgtgt	ttgatc	cagcgg	aac	ccc	cag	ctc	tgtgt
Val Leu	Ile Gln	Arg Asn	Pro Gln	Leu Cys	Tyr Gln	Asp Thr	Ile Leu
	155		160			165	
tggtgt	aag	gac	atc	ttc	cac	aag	aac
Trp Lys	Asp Ile	Phe His	Lys Asn	Asn Asn	Gln Leu	Ala Leu	Thr Leu
	170		175			180	
							702

Figure 8B

gac acc aac cgc tct cgg gcc tgc cac ccc tgt tct ccg atg tgt aag Asp Thr Asn Arg Ser Arg Ala Cys His Pro Cys Ser Pro Met Cys Lys 185 190 195 200	750
ggc tcc cgc tgc tgg gga gag agt tct gag gat tgt cag agc ctg acg Gly Ser Arg Cys Trp Gly Glu Ser Ser Glu Asp Cys Gln Ser Leu Thr 205 210 215	798
cgc act gtc tgt gcc ggt ggc tgt gcc cgc tgc aag ggg cca ctg ccc Arg Thr Val Cys Ala Gly Gly Cys Ala Arg Cys Lys Gly Pro Leu Pro 220 225 230	846
act gac tgc tgc cat gag cag tgt gct gcc ggc tgc acg ggc ccc aag Thr Asp Cys Cys His Glu Gln Cys Ala Ala Gly Cys Thr Gly Pro Lys 235 240 245	894
cac tct gac tgc ctg gcc tgc ctc cac ttc aac cac agt ggc atc tgt His Ser Asp Cys Leu Ala Cys Leu His Phe Asn His Ser Gly Ile Cys 250 255 260	942
gag ctg cac tgc cca gcc ctg gtc acc tac aac aca gac acg ttt gag Glu Leu His Cys Pro Ala Leu Val Thr Tyr Asn Thr Asp Thr Phe Glu 265 270 275 280	990
tcc atg ccc aat ccc gag ggc cgg tat aca ttc ggc gcc agc tgt gtg Ser Met Pro Asn Pro Glu Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val 285 290 295	1038
act gcc tgt ccc tac aac tac ctt tct acg gac gtg gga tcc tgc acc Thr Ala Cys Pro Tyr Asn Tyr Leu Ser Thr Asp Val Gly Ser Cys Thr 300 305 310	1086
ctc gtc tgc ccc ctg cac aac caa gag gtg aca gca gag gat gga aca Leu Val Cys Pro Leu His Asn Gln Glu Val Thr Ala Glu Asp Gly Thr 315 320 325	1134
cag cgg tgt gag aag tgc agc aag ccc tgt gcc cga gtg tgc tat ggt Gln Arg Cys Glu Lys Cys Ser Lys Pro Cys Ala Arg Val Cys Tyr Gly 330 335 340	1182
ctg ggc atg gag cac ttg cga gag gtg agg gca gtt acc agt gcc aat Leu Gly Met Glu His Leu Arg Glu Val Arg Ala Val Thr Ser Ala Asn 345 350 355 360	1230
atc cag gag ttt gct ggc tgc aag aag atc ttt ggg agc ctg gca ttt Ile Gln Glu Phe Ala Gly Cys Lys Lys Ile Phe Gly Ser Leu Ala Phe 365 370 375	1278
ctg ccg gag agc ttt gat ggg gac cca gcc tcc aac act gcc ccg ctc Leu Pro Glu Ser Phe Asp Gly Asp Pro Ala Ser Asn Thr Ala Pro Leu 380 385 390	1326
cag cca gag cag ctc caa gtg ttt gag act ctg gaa gag atc aca ggt Gln Pro Glu Gln Leu Gln Val Phe Glu Thr Leu Glu Glu Ile Thr Gly 395 400 405	1374

Figure 8C

tac cta tac atc tca gca tgg ccg gac agc ctg cct gac ctc agc gtc Tyr Leu Tyr Ile Ser Ala Trp Pro Asp Ser Leu Pro Asp Leu Ser Val 410 415 420	1422
ttc cag aac ctg caa gta atc cgg gga cga att ctg cac aat ggc gcc Phe Gln Asn Leu Gln Val Ile Arg Gly Arg Ile Leu His Asn Gly Ala 425 430 435 440	1470
tac tcg ctg acc ctg caa ggg ctg ggc atc agc tgg ctg ggg ctg cgc Tyr Ser Leu Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu Gly Leu Arg 445 450 455	1518
tca ctg agg gaa ctg ggc agt gga ctg gcc ctc atc cac cat aac acc Ser Leu Arg Glu Leu Gly Ser Gly Leu Ala Leu Ile His His Asn Thr 460 465 470	1566
cac ctc tgc ttc gtg cac acg gtg ccc tgg gac cag ctc ttt cgg aac His Leu Cys Phe Val His Thr Val Pro Trp Asp Gln Leu Phe Arg Asn 475 480 485	1614
ccg cac caa gct ctg ctc cac act gcc aac cgg cca gag gac gag tgt Pro His Gln Ala Leu Leu His Thr Ala Asn Arg Pro Glu Asp Glu Cys 490 495 500	1662
gtg ggc gag ggc ctg gcc tgc cac cag ctg tgc gcc cga ggg cac tgc Val Gly Glu Gly Leu Ala Cys His Gln Leu Cys Ala Arg Gly His Cys 505 510 515 520	1710
tgg ggt cca ggg ccc acc cag tgt gtc aac tgc agc cag ttc ctt cgg Trp Gly Pro Gly Pro Thr Gln Cys Val Asn Cys Ser Gln Phe Leu Arg 525 530 535	1758
ggc cag gag tgc gtg gag gaa tgc cga gta ctg cag ggg ctc ccc agg Gly Gln Glu Cys Val Glu Glu Cys Arg Val Leu Gln Gly Leu Pro Arg 540 545 550	1806
gag tat gtg aat gcc agg cac tgt ttg ccg tgc cac cct gag tgt cag Glu Tyr Val Asn Ala Arg His Cys Leu Pro Cys His Pro Glu Cys Gln 555 560 565	1854
ccc cag aat ggc tca gtg acc tgt ttt gga ccg gag gct gac cag tgt Pro Gln Asn Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys 570 575 580	1902
gtg gcc tgt gcc cac tat aag gac cct ccc ttc tgc gtg gcc cgc tgc Val Ala Cys Ala His Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg Cys 585 590 595 600	1950
ccc agc ggt gtg aaa cct gac ctc tcc tac atg ccc atc tgg aag ttt Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe 605 610 615	1998

Figure 8D

cca gat gag gag ggc gca tgc cag cct tgc ccc atc aac tgc acc cac Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys Thr His 620 625 630	2046
tcc tgt gtg gac ctg gat gac aag ggc tgc ccc gcc gag cag aga gcc Ser Cys Val Asp Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln Arg Ala 635 640 645	2094
agc cct ctg acg tcc atc gtc tct gcg gtg gtt ggc att ctg ctg gtc Ser Pro Leu Thr Ser Ile Val Ser Ala Val Val Gly Ile Leu Leu Val 650 655 660	2142
gtg gtc ttg ggg gtg gtc ttt ggg atc ctc atc aag cga cgg cag cag Val Val Leu Gly Val Val Phe Gly Ile Leu Ile Lys Arg Arg Gln Gln 665 670 675 680	2190
aag atc cgg aag tac acg atg cgg aga ctg ctg cag gaa acg gag ctg Lys Ile Arg Lys Tyr Thr Met Arg Arg Leu Leu Gln Glu Thr Glu Leu 685 690 695	2238
gtg gag ccg ctg aca cct agc gga gcg atg ccc aac cag gcg cag atg Val Glu Pro Leu Thr Pro Ser Gly Ala Met Pro Asn Gln Ala Gln Met 700 705 710	2286
cgg atc ctg aaa gag acg gag ctg agg aag gtg aag gtg ctt gga tct Arg Ile Leu Lys Glu Thr Glu Leu Arg Lys Val Lys Val Leu Gly Ser 715 720 725	2334
ggc gct ttt ggc aca gtc tac aag ggc atc tgg atc cct gat ggg gag Gly Ala Phe Gly Thr Val Tyr Lys Gly Ile Trp Ile Pro Asp Gly Glu 730 735 740	2382
aat gtg aaa att cca gtg gcc atc aaa gtg ttg agg gaa aac aca tcc Asn Val Lys Ile Pro Val Ala Ile Lys Val Leu Arg Glu Asn Thr Ser 745 750 755 760	2430
ccc aaa gcc aac aaa gaa atc tta gac gaa gca tac gtg atg gct ggt Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Gly 765 770 775	2478
gtg ggc tcc cca tat gtc tcc cgc ctt ctg ggc atc tgc ctg aca tcc Val Gly Ser Pro Tyr Val Ser Arg Leu Leu Gly Ile Cys Leu Thr Ser 780 785 790	2526
acg gtg cag ctg gtg aca cag ctt atg ccc tat ggc tgc ctc tta gac Thr Val Gln Leu Val Thr Gln Leu Met Pro Tyr Gly Cys Leu Leu Asp 795 800 805	2574
cat gtc cgg gaa aac cgc gga cgc ctg ggc tcc cag gac ctg ctg aac His Val Arg Glu Asn Arg Gly Arg Leu Gly Ser Gln Asp Leu Leu Asn 810 815 820	2622

Figure 8E

tgg tgt atg cag att gcc aag ggg atg agc tac ctg gag gat gtg cgg Trp Cys Met Gln Ile Ala Lys Gly Met Ser Tyr Leu Glu Asp Val Arg 825 830 835 840	2670
ctc gta cac agg gac ttg gcc gct cgg aac gtg ctg gtc aag agt ccc Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Ser Pro 845 850 855	2718
aac cat gtc aaa att aca gac ttc ggg ctg gct cgg ctg ctg gac att Asn His Val Lys Ile Thr Asp Phe Gly Leu Ala Arg Leu Leu Asp Ile 860 865 870	2766
gac gag aca gag tac cat gca gat ggg ggc aag gtg ccc atc aag tgg Asp Glu Thr Glu Tyr His Ala Asp Gly Gly Lys Val Pro Ile Lys Trp 875 880 885	2814
atg gcg ctg gag tcc att ctc cgc cgg cgg ttc acc cac cag agt gat Met Ala Leu Glu Ser Ile Leu Arg Arg Arg Phe Thr His Gln Ser Asp 890 895 900	2862
gtg tgg agt tat ggt gtg act gtg tgg gag ctg atg act ttt ggg gcc Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ala 905 910 915 920	2910
aaa cct tac gat ggg atc cca gcc cgg gag atc cct gac ctg ctg gaa Lys Pro Tyr Asp Gly Ile Pro Ala Arg Glu Ile Pro Asp Leu Leu Glu 925 930 935	2958
aag ggg gag cgg ctg ccc cag ccc ccc atc tgc acc att gat gtc tac Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr 940 945 950	3006
atg atc atg gtc aaa tgt tgg atg att gac tct gaa tgt cgg cca aga Met Ile Met Val Lys Cys Trp Met Ile Asp Ser Glu Cys Arg Pro Arg 955 960 965	3054
ttc cgg gag ttg gtg tct gaa ttc tcc cgc atg gcc agg gac ccc cag Phe Arg Glu Leu Val Ser Glu Phe Ser Arg Met Ala Arg Asp Pro Gln 970 975 980	3102
cgc ttt gtg gtc atc cag aat gag gac ttg ggc cca gcc agt ccc ttg Arg Phe Val Val Ile Gln Asn Glu Asp Leu Gly Pro Ala Ser Pro Leu 985 990 995 1000	3150
gac agc acc ttc tac cgc tca ctg ctg gag gac gat gac atg ggg Asp Ser Thr Phe Tyr Arg Ser Leu Leu Glu Asp Asp Asp Met Gly 1005 1010 1015	3195
gac ctg gtg gat gct gag gag tat ctg gta ccc cag cag ggc ttc Asp Leu Val Asp Ala Glu Glu Tyr Leu Val Pro Gln Gln Gly Phe 1020 1025 1030	3240

Figure 8F

ttc tgt cca gac cct gcc ccg ggc gct ggg ggc atg gtc cac cac Phe Cys Pro Asp Pro Ala Pro Gly Ala Gly Gly Met Val His His 1035 1040 1045	3285
agg cac cgc agc tca tct acc agg agt ggc ggt ggg gac ctg aca Arg His Arg Ser Ser Ser Thr Arg Ser Gly Gly Gly Asp Leu Thr 1050 1055 1060	3330
cta ggg ctg gag ccc tct gaa gag gag gcc ccc agg tct cca ctg Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala Pro Arg Ser Pro Leu 1065 1070 1075	3375
gca ccc tcc gaa ggg gct ggc tcc gat gta ttt gat ggt gac ctg Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly Asp Leu 1080 1085 1090	3420
gga atg ggg gca gcc aag ggg ctg caa agc ctc ccc aca cat gac Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His Asp 1095 1100 1105	3465
ccc agc cct cta cag cgg tac agt gag gac ccc aca gta ccc ctg Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu 1110 1115 1120	3510
ccc tct gag act gat ggc tac gtt gcc ccc ctg acc tgc agc ccc Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro 1125 1130 1135	3555
cag cct gaa tat gtg aac cag cca gat gtt cgg ccc cag ccc cct Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro 1140 1145 1150	3600
tcg ccc cga gag ggc cct ctg cct gct gcc cga cct gct ggt gcc Ser Pro Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala 1155 1160 1165	3645
act ctg gaa agg gcc aag act ctc tcc cca ggg aag aat ggg gtc Thr Leu Glu Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly Val 1170 1175 1180	3690
gtc aaa gac gtt ttt gcc ttt ggg ggt gcc gtg gag aac ccc gag Val Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu 1185 1190 1195	3735
tac ttg aca ccc cag gga gga gct gcc cct cag ccc cac cct cct Tyr Leu Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro His Pro Pro 1200 1205 1210	3780
cct gcc ttc agc cca gcc ttc gac aac ctc tat tac tgg gac cag Pro Ala Phe Ser Pro Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln 1215 1220 1225	3825

Figure 8G

gac cca cca gag cgg ggg gct cca ccc agc acc ttc aaa ggg aca	3870
Asp Pro Pro Glu Arg Gly Ala Pro Pro Ser Thr Phe Lys Gly Thr	
1230 1235 1240	
cct acg gca gag aac cca gag tac ctg ggt ctg gac gtg cca gtg	3915
Pro Thr Ala Glu Asn Pro Glu Tyr Leu Gly Leu Asp Val Pro Val	
1245 1250 1255	
tga accagaaggc caagtccgca gaagccctga tgtgtcctca gggagcaggg	3968
aaggcctgac ttctgctggc atcaagaggt gggagggccc tccgaccact tccaggggaa	4028
cctgccatgc caggaacctg tcctaaggaa ccttccttcc tgcttgagtt cccagatggc	4088
tggaaggggt ccagcctcgt tggaagagga acagcactgg ggagtctttg tggattctga	4148
ggccctgccc aatgagactc taggggtccag tggatgccac agcccagctt ggccctttcc	4208
ttccagatcc tgggtactga aagccttagg gaagctggcc tgagagggga agcggcccta	4268
agggagtgtc taagaacaaa agcgacccat tcagagactg tccctgaaac ctagtactgc	4328
cccccatgag gaaggaacag caatggtgtc agtatccagg ctttgtacag agtgcttttc	4388
tgtttagttt ttactttttt tgttttgttt ttttaaagac gaaataaaga cccaggggag	4448
aatgggtgtt gtatggggag gcaagtgtgg ggggtccttc tccacacca ctttgtccat	4508
ttgcaaatat attttggaaa ac	4530

Figure 9A

agccccaagc ttaccacctg caccgcggaga gctgtgtgtc acc atg tgg gtc ccg	55
Met Trp Val Pro	
1	
gtt gtc ttc ctc acc ctg tcc gtg acg tgg att ggt gct gca ccc ctc	103
Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile Gly Ala Ala Pro Leu	
5 10 15 20	
atc ctg tct cgg att gtg gga ggc tgg gag tgc gag aag cat tcc caa	151
Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu Lys His Ser Gln	
25 30 35	
ccc tgg cag gtg ctt gtg gcc tct cgt ggc agg gca gtc tgc ggc ggt	199
Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala Val Cys Gly Gly	
40 45 50	
gtt ctg gtg cac ccc cag tgg gtc ctc aca gct gcc cac tgc atc agg	247
Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala His Cys Ile Arg	
55 60 65	
aac aaa agc gtg atc ttg ctg ggt cgg cac agc ctg ttt cat cct gaa	295
Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu Phe His Pro Glu	
70 75 80	
gac aca ggc cag gta ttt cag gtc agc cac agc ttc cca cac ccg ctc	343
Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe Pro His Pro Leu	
85 90 95 100	
tac gat atg agc ctc ctg aag aat cga ttc ctc agg cca ggt gat gac	391
Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg Pro Gly Asp Asp	
105 110 115	
tcc agc cac gac ctc atg ctg ctc cgc ctg tca gag cct gcc gag ctc	439
Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu Pro Ala Glu Leu	
120 125 130	
acg gat gct gtg aag gtc atg gac ctg ccc acc cag gag cca gca ctg	487
Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln Glu Pro Ala Leu	
135 140 145	
ggg acc acc tgc tac gcc tca ggc tgg ggc agc att gaa cca gag gag	535
Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Glu	
150 155 160	
ttc ttg acc cca aag aaa ctt cag tgt gtg gac ctc cat gtt att tcc	583
Phe Leu Thr Pro Lys Lys Leu Gln Cys Val Asp Leu His Val Ile Ser	
165 170 175 180	
aat gac gtg tgt gcg caa gtt cac cct cag aag gtg acc aag ttc atg	631
Asn Asp Val Cys Ala Gln Val His Pro Gln Lys Val Thr Lys Phe Met	
185 190 195	

Figure 9B

ctg tgt gct gga cgc tgg aca ggg ggc aaa agc acc tgc tcg ggt gat Leu Cys Ala Gly Arg Trp Thr Gly Gly Lys Ser Thr Cys Ser Gly Asp 200 205 210	679
tct ggg ggc cca ctt gtc tgt aat ggt gtg ctt caa ggt atc acg tca Ser Gly Gly Pro Leu Val Cys Asn Gly Val Leu Gln Gly Ile Thr Ser 215 220 225	727
tgg ggc agt gaa cca tgt gcc ctg ccc gaa agg cct tcc ctg tac acc Trp Gly Ser Glu Pro Cys Ala Leu Pro Glu Arg Pro Ser Leu Tyr Thr 230 235 240	775
aag gtg gtg cat tac cgg aag tgg atc aag gac acc atc gtg gcc aac Lys Val Val His Tyr Arg Lys Trp Ile Lys Asp Thr Ile Val Ala Asn 245 250 255 260	823
ccc tga gcacccctat caacccccta ttgtagtaaa cttggaacct tggaaatgac Pro	879
caggccaaga ctcaagcctc cccagttcta ctgacctttg tccttaggtg tgaggtccag	939
ggttgctagg aaaagaaatc agcagacaca ggtgtagacc agagtgtttc ttaaattggtg	999
taattttgtc ctctctgtgt cctggggaat actggccatg cctggagaca tatcactcaa	1059
tttctctgag gacacagata ggatgggggtg tctgtgttat ttgtggggta cagagatgaa	1119
agaggggtgg gatccacact gagagagtgg agagtgacat gtgctggaca ctgtccatga	1179
agcactgagc agaagctgga ggcacaacgc accagacact cacagcaagg atggagctga	1239
aaacataacc cactctgtcc tggaggcact gggaagccta gagaaggctg tgagccaagg	1299
agggaggggtc ttcctttggc atgggatggg gatgaagtaa ggagagggac tggaccccct	1359
ggaagctgat tcactatggg gggaggtgta ttgaagtcct ccagacaacc ctcagatttg	1419
atgatttcct agtagaactc acagaaataa agagctgtta tactgtg	1466